SEQUENCE LISTING

(1) GENERAL INFORMATION:

5   (i) APPLICANT: Avi Ashkenazi

         (ii) TITLE OF INVENTION: Apo-2 Ligand
10
       (iii) NUMBER OF SEQUENCES: 8

        (iv) CORRESPONDENCE ADDRESS:
             (A) ADDRESSEE: Genentech, Inc.
15   (B) STREET: 1 DNA Way
             (C) CITY: South San Francisco
             (D) STATE: California
             (E) COUNTRY: USA
             (F) ZIP: 94080
20
         (v) COMPUTER READABLE FORM:
             (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
             (B) COMPUTER: IBM PC compatible
             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25   (D) SOFTWARE: WinPatin (Genentech)

        (vi) CURRENT APPLICATION DATA:
             (A) APPLICATION NUMBER:
             (B) FILING DATE:
30   (C) CLASSIFICATION:

      (viii) ATTORNEY/AGENT INFORMATION:
             (A) NAME: Marschang, Diane L.
             (B) REGISTRATION NUMBER: 35,600
35   (C) REFERENCE/DOCKET NUMBER: P0978P3

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 281 amino acids
10   (B) TYPE: Amino Acid
      (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr
 1               5                10                15

Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys
                20                25                30

Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met
                35                40                45

Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu
                50                55                60

Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser
                65                70                75

Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys
                80                85                90

Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
                95               100               105
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    Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
                     110               115                 120

    Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 5                   125               130                 135

    Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
                     140               145                 150

10  Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
                     155               160                 165

    Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly
                     170               175                 180

15  Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
                     185               190                 195

    Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
                     200               205                 210

20  Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
                     215               220                 225

25  Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
                     230               235                 240

    Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
                     245               250                 255

30  Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
                     260               265                 270

    Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
35                   275                   280 281
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1042 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTCCTCACT GACTATAAAA GAATAGAGAA GGAAGGGCTT CAGTGACCGG 50

CTGCCTGGCT GACTTACAGC AGTCAGACTC TGACAGGATC ATGGCTATGA 100

TGGAGGTCCA GGGGGGACCC AGCCTGGGAC AGACCTGCGT GCTGATCGTG 150

ATCTTCACAG TGCTCCTGCA GTCTCTCTGT GTGGCTGTAA CTTACGTGTA 200

CTTTACCAAC GAGCTGAAGC AGATGCAGGA CAAGTACTCC AAAAGTGGCA 250

TTGCTTGTTT CTTAAAAGAA GATGACAGTT ATTGGGACCC CAATGACGAA 300

GAGAGTATGA ACAGCCCCTG CTGGCAAGTC AAGTGGCAAC TCCGTCAGCT 350

CGTTAGAAAG ATGATTTTGA GAACCTCTGA GGAAACCATT TCTACAGTTC 400

AAGAAAAGCA ACAAAATATT TCTCCCCTAG TGAGAGAAAG AGGTCCTCAG 450

AGAGTAGCAG CTCACATAAC TGGGACCAGA GGAAGAAGCA ACACATTGTC 500

TTCTCCAAAC TCCAAGAATG AAAAGGCTCT GGGCCGCAAA ATAAACTCCT 550

GGGAATCATC AAGGAGTGGG CATTCATTCC TGAGCAACTT GCACTTGAGG 600

AATGGTGAAC TGGTCATCCA TGAAAAGGG TTTTACTACA TCTATTCCCA 650

AACATACTTT CGATTTCAGG AGGAAATAAA AGAAACACA AAGAACGACA 700

AACAAATGGT CCAATATATT TACAAATACA CAAGTTATCC TGACCCTATA 750

TTGTTGATGA AAAGTGCTAG AAATAGTTGT TGGTCTAAAG ATGCAGAATA 800

TGGACTCTAT TCCATCTATC AAGGGGGAAT ATTTGAGCTT AAGGAAAATG 850

ACAGAATTTT TGTTTCTGTA ACAAATGAGC ACTTGATAGA CATGGACCAT 900

GAAGCCAGTT TTTTCGGGGC CTTTTTAGTT GGCTAACTGA CCTGGAAAGA 950

AAAAGCAATA ACCTCAAAGT GACTATTCAG TTTTCAGGAT GATACACTAT 1000

GAAGATGTTT CAAAAAATCT GACCAAAACA AACAAACAGA AA 1042

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 390 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGACCCCAA TGACGAAGAG AGTATGAACA GCCCCTGCTG GCAAGTCAAG 50

TGGCAACTCC GTCAGCTCGT TAGAAAGATG ATTTTGAGAA CCTCTGAGGA 100

AACCATTTCT ACAGTTCAAG AAAAGCAACA AAATATTTCT CCCCTAGTGA 150

GAGAAAGAGG TCCTCAGAGA GTAGCAGCTC ACATAACTGG GACCAGAGGA 200

AGAAGCAACA CATTGTCTTC TCCAAACTCC AAGAATGAAA AGGCTCTGGG 250

CCGCAAAATA AACTCCTGGG AATCATCAAG GAGTGGGCAT TCATTCCTGA 300

GCAACTTGCA CTTGAGGAAT GGTGAACTGG TCATCCATGA AAAAGGGTTT 350

TACTACATCT ATTCCCAAAC ATACTTTCGA TTTCAGGAGG 390

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGACGAAGAG AGTATGAACA GCCCCTGCTG GCAAGTCAAG TGGCAACTCC 50

GTCAGCTCGT 60

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 60 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGAACTGG TCATCCATGA AAAAGGGTTT TACTACATCT ATTCCCAAAC 50

ATACTTTCGA 60

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 13 amino acids
            (B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

    Ser Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1   5   10   13

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

    Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn
         1   5   10   15

    Arg Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln
20   25   27

    (2) INFORMATION FOR SEQ ID NO:8:

        (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly His His His His His His His His His Ser Ser Gly
1   5   10   15

His Ile Asp Asp Asp Asp Lys His Met
                    20   24